

Identifying Associations between Neutrophil Response Status and Protein Expression Pre- and Post- Woodsmoke Exposure

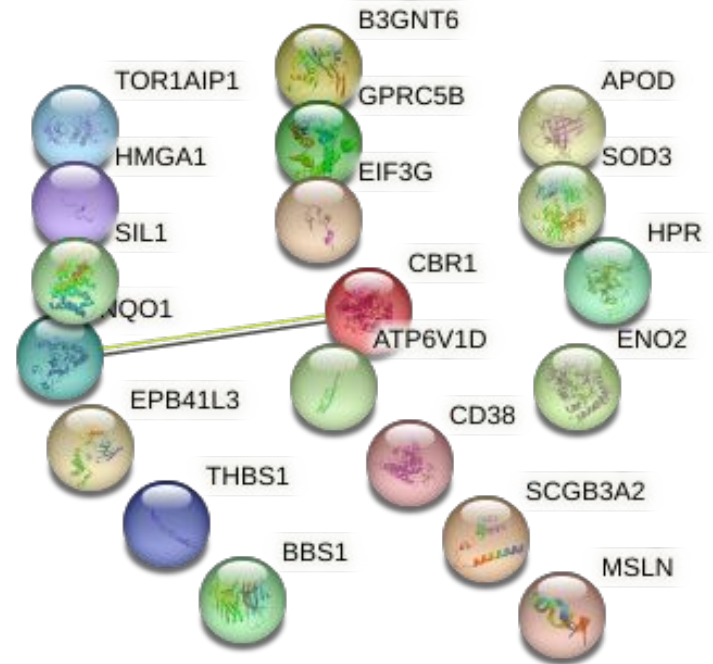
PREHEAT Retreat
Erin McNell & Caty Cobos-Urbe

Differentially Expressed Proteins: **Pre-Exposure**

19 differentially expressed proteins

Very few associations between proteins

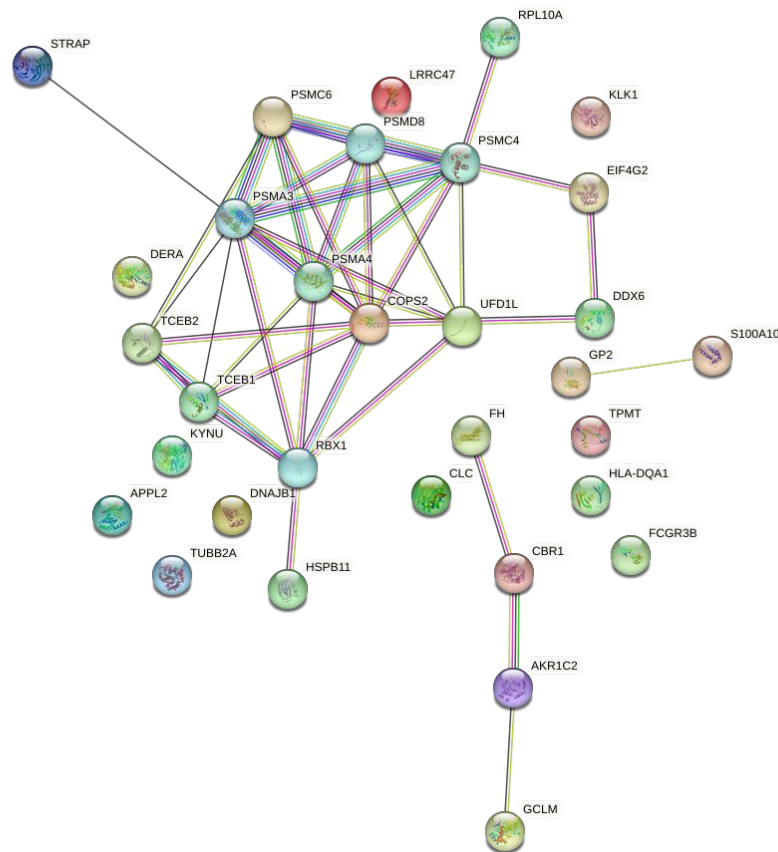
	Statistic <dbl>	Pval <dbl>
SOD3	2.688326	0.01301883
THBS1	2.702746	0.01408771
MSLN	2.668974	0.01649394
ATP6V1D	2.533069	0.01899311
SIL1	2.484272	0.02011033
GPRC5B	2.490424	0.02031310



Differentially Expressed Proteins: **Post-Exposure**

30 differentially expressed proteins
Many associations between proteins

Biological Process (Gene Ontology)	
GO-term	description
GO:0008152	Metabolic process
GO:0044238	Primary metabolic process
GO:0071704	Organic substance metabolic process
GO:0006807	Nitrogen compound metabolic process
GO:1901564	Organonitrogen compound metabolic process
GO:0042221	Response to chemical
GO:0010468	Regulation of gene expression
GO:0006950	Response to stress
GO:0048583	Regulation of response to stimulus
GO:0010033	Response to organic substance
GO:0034641	Cellular nitrogen compound metabolic process
GO:0070887	Cellular response to chemical stimulus
GO:0006725	Cellular aromatic compound metabolic process
GO:0033554	Cellular response to stress
GO:1901575	Organic substance catabolic process
GO:0044248	Cellular catabolic process
GO:0006508	Proteolysis



Machine Learning:

Predicting Responder Status using Linear Model

Goal: Predict responder status using protein concentration data

Non-Responder = 0

Responder = 1

```
> logit_pred
      35      26      16      40      49      44      48
-1.3324408 -2.2723814  0.6255314 -0.7032659 -0.9644781  1.8307484  0.1097371
```

```
> lr_acc
[1] 0.5
```

Accuracy: 50%